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MIPS

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Aug 7 19:25:00 1999; MasPar time 1828.51 Seconds
1515.934 Million cell updates/sec
Total output not generated.

Title: >US-08-287-669-18
Description: (4501-5500) from US08287669.seq (6 of 10)
Perfect Score: 1000
N.A. Sequence: 4501 GGCTCATGATATATGAA.....ACCAAAAGAAACCGAAAA 5500
Comp: CGGAGTAGTATTATGCTT.....TGGTTTCTTTGGGCTTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 646147 seqs, 138593633 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb158
1:em_bal 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2
7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_v1
genbank111
17:gb_bal 18:gb_ba2 19:gb_btg1 20:gb_htg2 21:gb_in1
22:gb_in2 23:gb_om 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl1
28:gb_pl2 29:gb_pr1 30:gb_pr2 31:gb_pr3 32:gb_ro
33:gb_st 34:gb_sts 35:gb_sy 36:gb_un 37:gb_v1

Statistics: Mean 11.336; Variance 8.769; scale 1.293

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1000	100.0	7653	21	CELCE3A	Caenorhabditis elegans	0.00e+00
2	950	95.0	39908	21	CEC48D1	Caenorhabditis elegans	0.00e+00
3	936	93.6	31495	19	CEY57H2	Caenorhabditis elegans	0.00e+00
4	78	7.8	26788	21	CEL704B8	Caenorhabditis elegans	1.59e-17
5	73	7.3	299300	20	AC006881	Caenorhabditis elegans	1.46e-19
6	70	7.0	36256	21	CEY38A6	Caenorhabditis elegans	1.14e-17
7	70	7.0	257817	19	AC006909	Caenorhabditis elegans	1.14e-17
8	70	7.0	326074	19	CEY44A6	Caenorhabditis elegans	1.14e-17
9	69	6.9	143092	21	CEY17G7B	Caenorhabditis elegans	3.43e-17
10	69	6.9	207139	19	CEY17G7	Caenorhabditis elegans	3.43e-17
11	68	6.8	12355	19	AC006678	Caenorhabditis elegans	1.02e-16
12	67	6.7	22333	21	CELCO2F5	C. elegans cosmid C02F	3.06e-16
13	66	6.6	19292	21	CEY76A2A	Caenorhabditis elegans	9.09e-16

14	66	6.6	34191	21	CER102	Caenorhabditis elegans	9.09e-16
15	66	6.6	245805	20	AC006752	Caenorhabditis elegans	9.09e-16
16	66	6.6	269082	19	CEX76A2	Caenorhabditis elegans	9.09e-16
17	65	6.5	34700	21	CEC44B9	Caenorhabditis elegans	2.70e-15
18	65	6.5	35165	21	CELC56C10	Caenorhabditis elegans	2.70e-15
19	65	6.5	38990	21	CEY36D3	Caenorhabditis elegans	2.70e-15
20	65	6.5	191857	19	CEY32B12	Caenorhabditis elegans	2.70e-15
21	64	6.4	33883	21	CELK03E5	Caenorhabditis elegans	2.70e-15
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36	63	6.3	291821	19	CEY48E1	Caenorhabditis elegans	2.35e-14
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43	61	6.1	36120	21	CEYF56D1	Caenorhabditis elegans	2.02e-13
44	61	6.1	14763	19	CEY40D7	Caenorhabditis elegans	2.02e-13
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ALIGNMENTS

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ACCESSION	L29052							
VERSION	L29052.1	GI:456416						
KEYWORDS		cell death protein; interleukin-1 beta converting enzyme.						
SOURCE		Caenorhabditis elegans (strain N2) DNA.						
ORGANISM		Caenorhabditis elegans						
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Caenorhabditis.						
AUTHORS		Yuan, J., Shahan, S., Ledoux, S., Ellis, H.M. and Horvitz, H.						
TITLE		The C. elegans cell death gene ced-3 encodes a protein similar to mammalian interleukin-1b-converting enzyme						
JOURNAL		Cell 75, 641-652 (1993)						
MEDLINE		94061982						
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intron

Key

intron

5

intron

•

100

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ORIGIN	2498 t		

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	Best Local Similarity 100.0%;	Pred. No. 0.00e+00;			
	Matches 1000;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	4501	GCCTCATATAAATATGACACTTTTGACAGATGCCAACACGGATGTCACCAAGCCG	4560		
Db	4561	ACAAGGACAACTCTTACCAATTTTCTTCAGATGCATGGGCTATACGGTTATTTCGAAGGACA	4620		
QY	4561	ACAAGGACAACTCTTACCAATTTTCTTCAGATGCATGGGCTATACGGTTATTTCGAAGGACA	4620		
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NID	g1627677				
VERSION	Z81049.1	GI:1627677			
KEYWORDS	HTG.				
SOURCE	Caenorhabditis elegans.				
ORGANISM	Caenorhabditis elegans				
	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;				
	Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.				
REFERENCE	1 (bases 1 to 3908)				
AUTHORS	Burton,J.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jcs@sanger.ac.uk or rw@ematode.wustl.edu				

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 Cp 7429 ATTGATCCCGCAAAAAT 7411

RESULT 10
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 DEFINITION Saccharomyces cerevisiae chromosome XVI cosmid 8209/8002.
 ACCESSION U43503 U00094
 NID g1163087
 VERSION U43503.1 GI:1163087
 KEYWORDS Schizosaccharomyces pombe C18B11.10 homolog; NIP29; Aspergillus
 oryzae ribonuclease T2 homolog; MEI5; H.sapiens GT197 EST homolog;
 DBP1; S.kluuyverii k-ORF1 homolog; IDI1; C.elegans CF4366.4 product
 homolog; BEK3; E.coli 2-hydroxyacid dehydrogenase homolog; TRNAMet;

SOURCE ORGANISM
 ORGANISM
 Carl; S.cerevisiae Pho81p homolog; Clostridium pasteurianum protein
 homolog.
 baker's yeast.
 Saccharomyces cerevisiae
 Eukaryotae; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
 Saccharomycetaceae; Saccharomycetes.
 1 (bases 1 to 38590)
 Sunrada, R.A. and Cooper, T.G.
 Nucleotide sequence of the Saccharomyces cerevisiae arginase gene
 (CAR1) and its transcription under various physiological conditions
 J. Bacteriol. 160 (3), 1078-1087 (1984)
 85054621
 2 (bases 1 to 38590)
 Anderson, M.S., Muehlbacher, M., Street, I.P., Proffitt, J. and
 Poulter, C.D., Isopentenyl diphosphate:dimethylallyl diphosphate isomerase. An
 improved purification of the enzyme and isolation of the gene from
 Saccharomyces cerevisiae
 J. Biol. Chem. 264 (32), 19169-19175 (1989)
 90037050
 3 (bases 1 to 38590)
 Jamieson, D.J. and Beggs, J.D.
 A suppressor of yeast spp81/ded1 mutations encodes a very simil
 putative ATP-dependent RNA helicase
 Mol. Microbiol. 5 (4), 805-812 (1991)
 91312117
 4 (bases 1 to 38590)
 Zheng, Y., Cerlione, R. and Bender, A.
 Control of the yeast bud-site assembly GTPase Cdc42. Catalysis
 guanine nucleotide exchange by Cdc24 and stimulation of GTPase
 activity by Bem3
 J. Biol. Chem. 269 (4), 2369-2372 (1994)
 94131990
 5 (bases 1 to 38590)
 Bussey, H., Storms, R.K., Ahmed, A., Albermann, K., Allen, E.,
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 Wedler, H., Winnett, E., Zhong, W.W., Zollner, A., Vo, D.H. and Hani, J.
 The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI
 Nature 387 (6632 Suppl), 103-105 (1997)
 97313271
 6 (bases 1 to 38590)
 Schlensstedt, G. and Silver, P.A.
 Unpublished
 7 (bases 1 to 38590)
 Hall, J., Ahmed, A., Bussey, H., Fortin, N., Friesen, J.D.,
 Storms, R.K., Vo, D.H., Wang, Y. and Winnett, E.
 The sequence of Saccharomyces cerevisiae chromosome XVI left arm
 Unpublished
 8 (bases 1 to 38590)
 Weber, L. and Byers, B.E.
 mei5, a novel meiotic mutation
 J. Bacteriol. 173 (1992)
 9 (bases 1 to 38590)
 Bussey, H.
 Direct Submission
 Submitted (15-DEC-1995) Howard Bussey, McGill University, Biology,
 1205 Dr. Penfield Ave., Montreal, Quebec H3A 1B1, Canada
 10 (bases 1 to 38590)
 Jia, Y. and Cherry, J.M.
 Direct Submission

JOURNAL Submitted (02-SEP-1997) Department of Genetics, Stanford University, Saccharomyces Genome Database, Stanford, CA 94305-5120, USA

COMMENT

Curated by:
Saccharomyces Genome Database
URL: <http://genome-www.stanford.edu/>
e-mail: yeast-curator@genome.stanford.edu

All CDS of 100 or more codons have been analyzed. CDS that are overlapped by larger CDS are not included. Cosmid 8209/8002 is overlapped at the beginning by cosmid 9545, and at the end by cosmid 8059.

FEATURES

source

Location/Qualifiers

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gene

CDS

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GMPPNRSNLDORIBERTSPVTRDKAFSONVDDQRLKYLRLIVYDQGVINDLTS
RITRLESFILNISDRGKNFASLEHSRSFGFPNKTYIGLQMGGLIENDMPYRRSSD
NINKEGAREDRSSQIHENESTEDILKILSSSFHN"

gene

complement(7784..9088)
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complement(7784..9088)
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CDS

/note="Similar to Aspergillus oryzae encoded ribonuclease
T2 precursor, Swiss-Prot Accession Number P10281"

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GNCISTIRPECYTERGANSVDRKRAVDYFRITYNLEKLDFTSELEKNNIVPSVDNS
YSLEQIEALSKEFEKGVFICGDHNSLNEWYVYHLSLSEMFYMDSLARTN
CKKDGIKFPFGVYVTRRRPNKGRYRGVRLSNINNGDQMGFLKNGHMSQGT
ANYELIKPGYNYLRTNQGCDIISSSNELVCFKRNKIDAGQDFDPTKGGDGYIG
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gene

complement(9369..10910)
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CDS

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Query Match 4.2% Score 19; DB 28; Length 38590;
Best Local Similarity 100.0%; Pred.No. 3.38e+00;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4612 ATGCTTCTATCAACAAAAT 4630

QY 7343 ATGCTTCTATCAACAAAAT 7361

RESULT 11

LOCUS HS657J8 98954 bp DNA PRI 11-DEC-1998
DEFINITION Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3
Contains GSS, complete sequence.

ACCESSION AL034407

NID 93980437

VERSION AL034407.1 GI:3980437

KEYWORDS HTG.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 98954)

AUTHORS Grafham,D.

TITLE Direct Submission

JOURNAL Submitted (07-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire,

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FVDAPITKDNLTGRMLLTIRDPAKHSHGSDSAILVILSHGEENVIIIGVDDIPITSTHEI
YDLNANAPRLANKPKIVQACRGERDNGFPVLDSDVGPAPFLRGRWDRDGLF
NFGCVRPQVQWRKKPSQADILIRIATIAQVSWNSANGSWFLOACEVFEVSTHAK
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7013..7652
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Query Match 100.0%; Score 1000; DB 21; Length 7653;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 4501 GCCTCATATAAATGAACACATTTGAGCAGATGCCAACACGGAATGGTACCAAGGCCG 4560
Qy 4501 GCCTCATATAAATGAACACATTTGAGCAGATGCCAACACGGAATGGTACCAAGGCCG 4560
Db 4561 ACAAGGACAATCTTACCAATTTGTCAGATGCTATACCGGCTATACGGTATTGCGATTITGGC 4620
Qy 4561 ACAAGGACAATCTTACCAATTTGTCAGATGCTATACCGGCTATACGGTATTGCGATTITGGC 4620
Db 4621 ATCTGACGGGAAGGTACGGGAATATTATACCGAAGCGGAATTTGCCATTITGGC 4680
Qy 4621 ATCTGACGGGAAGGTACGGGAATATTATACCGAAGCGGAATTTGCCATTITGGC 4680

Db 4681 CCGAAATGTGGCCCGCGTCTCGACACGACAAATTTGTGTAAATGCAAAATGTATAAT 4740
Qy 4681 CCGAAATGTGGCCCGCGTCTCGACACGACAAATTTGTGTAAATGCAAAATGTATAAT 4740
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Qy 4741 TTTGCAAAAACAAAATTTTGAACCTTCGCGGAAAATGATTTACCTAGTTTCGAAATTTTC 4800
Db 4801 GTTTTTCCGGCTACATATGTTTTCTTTCTAGTTTCTATATAATTTTGATGTAAAA 4860
Qy 4801 GTTTTTCCGGCTACATATGTTTTCTTTCTAGTTTCTATATAATTTTGATGTAAAA 4860
Db 4861 ACCGTTTGTAAATTTTCAGACAAATTTTCGCATACAAAATTTGATAGCAGAAATCAAT 4920
Qy 4861 ACCGTTTGTAAATTTTCAGACAAATTTTCGCATACAAAATTTGATAGCAGAAATCAAT 4920
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Qy 4921 TTTCTGAATTTTCAAAATTTATCCAAAATGCACAAATTTAAATTTGTGAAATTTGGCAAC 4980
Db 4981 GGTGTTTCAATATGAATTTTAAACCTTTTAAACCTTTTAAACCTTTTAAACCTTTTAA 5040
Qy 4981 GGTGTTTCAATATGAATTTTAAACCTTTTAAACCTTTTAAACCTTTTAAACCTTTTAA 5040
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Qy 5041 AAATCAAAACACGTCACAAATTTCAAAATTTCAAAAGTTTATTCATCCGATTTGTTTATTTTG 5100
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Qy 5221 ACAGCTTCGAGAGTTTGAATTTACAGTACTCTTAAAGGCGACACCCATTTGCATTGG 5280
Db 5281 ACCAAAATTTGTGTCGTCGAGACAGGATGCGTATGTTTGTGCAAAAATTTGCACCAT 5340
Qy 5281 ACCAAAATTTGTGTCGTCGAGACAGGATGCGTATGTTTGTGCAAAAATTTGCACCAT 5340
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Qy 5341 TGGACAAATAAACCCTTCAATCACCACCAAAAGTAAATTTGAAATCTTCGAAAGGCCAAAA 5400
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Qy 5401 ATTCAAAAATTTGCGAATTTTCGATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 5460
Db 5461 AAATCAATTTTTCGCAAAATATACCAAAAGAACCCGAAAA 5500
Qy 5461 AAATCAATTTTTCGCAAAATATACCAAAAGAACCCGAAAA 5500

RESULT 2
LOCUS CEC48D1 39908 bp DNA INV 23-NOV-1998
DEFINITION Caenorhabditis elegans cosmid C48D1, complete sequence.
ACCESSION Z81049
NID 91627677
VERSION 281049.1 GI:1627677
KEYWORDS HTG.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 39908)
AUTHORS Burton,J.
TITLE Direct Submision
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